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 FASTA searches a protein or DNA sequence data bank  
 version 3.4t10 Dec 12, 2001

Please cite:

W. R. Pearson &amp; D. J. Lipman PNAS (1988) 85:2444-2448

/tmp/WWW/get\_linkdb\_fasta.25159/b3823: 122 aa  
 >eco:b3823 yigJ; hypothetical 22.5 kD protein in recQ-mlD Intergenic region (A)  
 vs /bio/db/fasta/genes/genes library  
 searching /bio/db/fasta/genes/genes library

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  102  197  134:*
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  106  123  80:*
  108  102  62:*
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BEST AVAILABLE COPY

110	101	48: <sup>*</sup>	===== <sup>*</sup> ====
112	63	37: <sup>*</sup>	===== <sup>*</sup> ====
114	44	29: <sup>*</sup>	===== <sup>*</sup> ====
116	38	22: <sup>*</sup>	===== <sup>*</sup> ====
118	32	17: <sup>*</sup>	===== <sup>*</sup> ====
120	26	12: <sup>*</sup>	===== <sup>*</sup> ====

257957986 residues in 729837 sequences  
 statistics extrapolated from 60000 to 729458 sequences  
 Expectation\_n fit: rho(ln(x)) = 3.2816 +/- 0.000188; nu= 15, 2431 +/- 0.011  
 mean\_var=57.4751 +/- 11.689, 0's: 0 Z-trim: 3 B-trim: 3787 in 1/58  
 Lambda= 0.1692  
 Kolmogorov-Smirnov statistic: 0.0430 (N=29) at 50

FASTA (3.44 Dec 2001) function [optimized, BL50 matrix (15:-5)] ktup: 2  
join: 36, opt: 24, open/ext: -10/-2, width: 16 |

Scan time: 89.390

The best scores are

**Top 10**  **Clean**

Top 10  Clear Select operation

Exe

opt bits E(729837)

- |  |  |        |     |     |          |
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| <input checked="" type="checkbox"/> <b>eco:b3823</b>   | yigJ; hypothetical 22.5 kD protein in recQ-pldB  | ( 122) | 792 | 200 | 5e-51    |
| <input checked="" type="checkbox"/> <b>ecj:JW3797</b>  | yigJ; Amino acid exporter (threonine)            | ( 155) | 792 | 201 | 6. 7e-51 |
| <input checked="" type="checkbox"/> <b>ecs:ECs4753</b> | threonine efflux protein [KO:K03329]             | ( 206) | 792 | 201 | 6. 7e-51 |
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| <input checked="" type="checkbox"/> <b>sfl:SF3901</b>  | rhtC; threonine efflux protein                   | ( 206) | 786 | 199 | 1. 9e-50 |
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| <input checked="" type="checkbox"/> <b>stm:STM3959</b> | rhtC; RhtB family, threonine efflux protein      | ( 206) | 717 | 182 | 2. 2e-45 |
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| <input type="checkbox"/> <b>yem:YP3216</b>             | rhtC; threonine efflux protein                   | ( 206) | 560 | 144 | 7. 5e-34 |
| <input type="checkbox"/> <b>ypk:y0398</b>              | threonine efflux protein                         | ( 206) | 560 | 144 | 7. 5e-34 |
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| <input type="checkbox"/> <b>bha:BH2932</b>             | unknown conserved protein                        | ( 210) | 229 | 63  | 1. 6e-09 |
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| <input type="checkbox"/> <b>sme:SMc02484</b>           | putative amino acid efflux transmembrane prot    | ( 214) | 210 | 59  | 4e-08    |
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| <input type="checkbox"/> <b>sty:STY0397</b>            | RhtC-like transporter                            | ( 210) | 194 | 55  | 5. 9e-07 |

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<input type="checkbox"/> baa:BX80078	amino acid efflux protein, (pX02-63)	( 205)	150	44 0. 00099
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<input type="checkbox"/> vpa:VP1743	conserved hypothetical protein	( 211)	150	44 0. 001

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<input type="checkbox"/> aci:ACIAD3166 putative amino-acid efflux transmembrane protein	( 211)	150	44	0.001
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<input type="checkbox"/> ppu:PP0699 transporter, LysE family	( 204)	130	39	0.029
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<input type="checkbox"/> son:S03657	transporter, LysE family	( 229)	115	36	0. 39

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<input type="checkbox"/> <a href="#">vvy:VVA1119</a>	putative threonine efflux protein	( 210)	114	35	0.44
<input type="checkbox"/> <a href="#">vvu:VV20571</a>	putative threonine efflux protein	( 210)	114	35	0.44
<input type="checkbox"/> <a href="#">ypa:YPA0532</a>	conserved hypothetical protein	( 210)	114	35	0.44
<input type="checkbox"/> <a href="#">sme:SMc02981</a>	putative amino acid efflux transmembrane prot	( 211)	113	35	0.53
<input type="checkbox"/> <a href="#">gef:CE1357</a>	lysE; lysine exporter protein	( 235)	113	35	0.56
<input type="checkbox"/> <a href="#">vvu:VV20771</a>	putative threonine efflux protein	( 187)	112	35	0.58
<input type="checkbox"/> <a href="#">aci:ACIAD0173</a>	rhtB; homoserine/homoserine lactone efflux p	( 208)	112	35	0.62
<input type="checkbox"/> <a href="#">bha:BH3495</a>	dihydrodipicolinate reductase	( 208)	112	35	0.62
<input type="checkbox"/> <a href="#">atu:Atu3460</a>	rhtB; RhtB family transporter	( 210)	112	35	0.62
<input type="checkbox"/> <a href="#">pst:PSPT01885</a>	efflux protein, LysE family	( 213)	112	35	0.63
<input type="checkbox"/> <a href="#">yyy:VVA1237</a>	putative threonine efflux protein	( 215)	112	35	0.63
<input type="checkbox"/> <a href="#">sme:SMc00642</a>	hypothetical transmembrane protein	( 296)	113	35	0.63
<input type="checkbox"/> <a href="#">vpa:VPA1232</a>	conserved hypothetical protein	( 204)	111	35	0.72
<input type="checkbox"/> <a href="#">atc:AGR_L_2738</a>	conserved hypothetical protein	( 278)	112	35	0.73
<input type="checkbox"/> <a href="#">pae:PA5341</a>	hypothetical protein	( 206)	111	35	0.73
<input type="checkbox"/> <a href="#">cyl:CV4042</a>	probable amino acid efflux protein	( 209)	111	35	0.73
<input type="checkbox"/> <a href="#">sme:SMc03827</a>	putative amino acid efflux transmembrane prot	( 213)	111	35	0.74
<input type="checkbox"/> <a href="#">ojh:OB0964</a>	hypothetical conserved protein	( 171)	109	34	0.92

>>[eco:Z5344](#) yigJ; orf; Unknown function (122 aa)  
 initn: 792 initl: 792 opt: 792 Z-score: 1053.8 bits: 200.4 E(0) : 5e-51  
 Smith-Waterman score: 792; 100.000% identity (100.000% ungapped) in 122 aa overlap (1-122:1-122)

10	20	30	40	50	60	70	
eco:b3	MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTATARWGI	::::::::::					
eco:25	MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTATARWGI	::::::::::					
	10	20	30	40	50	60	70

80	90	100	110	120	
eco:b3	LIVETLAWFTVVASLFAFPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR	::::::::::			
eco:25	LIVETLAWFTVVASLFAFPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR	::::::::::			
	80	90	100	110	120

>>[eco:b3823](#) yigJ; hypothetical 22.6 kD protein in recQ-pldB inter (122 aa)  
 initn: 792 initl: 792 opt: 792 Z-score: 1053.8 bits: 200.4 E(0) : 5e-51  
 Smith-Waterman score: 792; 100.000% identity (100.000% ungapped) in 122 aa overlap (1-122:1-122)

10	20	30	40	50	60	70	
eco:b3	MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTATARWGI	::::::::::					
eco:b3	MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTATARWGI	::::::::::					
	10	20	30	40	50	60	70

80	90	100	110	120	
eco:b3	LIVETLAWFTVVASLFAFPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR	::::::::::			
eco:b3	LIVETLAWFTVVASLFAFPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR	::::::::::			
	80	90	100	110	120

>>[ecj:JW3797](#) yigJ; Amino acid exporter (threonine) (155 aa)  
 initn: 799 initl: 799 opt: 792 Z-score: 1052.7 bits: 200.6 E(0) : 5.7e-51  
 Smith-Waterman score: 792; 100.000% identity (100.000% ungapped) in 122 aa overlap (1-122:34-155)

Search Result: eco:b3823 -&gt; GENES

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10 20 30  
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLT  
::: ::::: :::::

10 20 30 40 50 60 70  
ecj:JW LGHDCAAWPAFDYRKNGLAAYADYGGRWLYLCM MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLT

40 50 60 70 80 90 100  
eco:b3 NLANPKAIIYFGSVFSLFVGDNVGTARWGIFALIIIVETLAWFTVVASLFA L P Q M R R G Y Q R L A K W D G F A  
::: ::::: :::::  
ecj:JW NLANPKAIIYFGSVFSLFVGDNVGTARWGIFALIIIVETLAWFTVVASLFA L P Q M R R G Y Q R L A K W D G F A  
80 90 100 110 120 130 140

110 120  
eco:b3 GALFAGFGIHLIISR  
::: ::::: :::::  
ecj:JW GALFAGFGIHLIISR  
150

>>ecs:ECs4753 threonine efflux protein (X0:K03329) (206 aa)  
initn: 799 initl: 799 opt: 792 Z-score: 1051.5 bits: 200.8 E 0 : 6.7e-51  
Smith-Waterman score: 792; 100.000% identity (100.000% ungapped) in 122 aa overlap (1-122:85-206)

10 20 30  
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL  
::: ::::: :::::  
ecs:EC MVWAGIALLGLHLIEKHAWLHTLIMVGGGLYLCL MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL  
50 60 70 80 90 100 110

40 50 60 70 80 90 100  
eco:b3 LTNLANPKAIIYFGSVFSLFVGDNVGTARWGIFALIIIVETLAWFTVVASLFA L P Q M R R G Y Q R L A K W D G  
::: ::::: :::::  
ecs:EC LTNLANPKAIIYFGSVFSLFVGDNVGTARWGIFALIIIVETLAWFTVVASLFA L P Q M R R G Y Q R L A K W D G  
120 130 140 150 160 170 180

110 120  
eco:b3 FAGALFAGFGIHLIISR  
::: ::::: :::::  
ecs:EC FAGALFAGFGIHLIISR  
190 200

>>sfx:S3854 yigJ: hypothetical protein (122 aa)  
initn: 786 initl: 786 opt: 786 Z-score: 1045.9 bits: 199.0 E 0 : 1.4e-50  
Smith-Waterman score: 786; 99.180% identity (99.180% ungapped) in 122 aa overlap (1-122:1-122)

10 20 30 40 50 60 70  
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLTNLANPKAIIYFGSVFSLFVGDNVGTARWGIFA  
::: ::::: :::::  
sfx:S3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLTNLANPKAIIYFGSVFSLFVGDNVGTTERWGIFA  
10 20 30 40 50 60 70

80 90 100 110 120  
eco:b3 LIIIVETLAWFTVVASLFA L P Q M R R G Y Q R L A K W D G F A G A F G I H L I S R  
::: ::::: :::::  
sfx:S3 LIIIVETLAWFTVVASLFA L P Q M R R G Y Q R L A K W D G F A G A F G I H L I S R  
80 90 100 110 120

>>sfx:SF3901 rhtC; threonine efflux protein (206 aa)  
initn: 793 initl: 793 opt: 786 Z-score: 1043.6 bits: 199.3 E 0 : 1.9e-50  
Smith-Waterman score: 786; 99.180% identity (99.180% ungapped) in 122 aa overlap (1-122:85-206)

10 20 30  
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL  
::: ::::: :::::  
sfx:SF MVWAGIALLGLHLIEKHAWLHTLIMVGGGLYLCL MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL  
50 60 70 80 90 100 110

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ZU04 09/00 H 19:33 MAI 分析付申請用  
U4-0-20; 014040M:送信(日本語モード)

WU42443015

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Search Result: eco:b3823 → GENES

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40	50	60	70	80	90	100
eco:b3 LTNLANPKAI YFGSVFSLFVGDNVGTARWG FAL  VETLAWFTVVASLFA PQMRRGYQRLAKW DG	.....	.....	.....	.....	.....	.....
120	130	140	150	160	170	180

110	120
eco:b3 FAGALFAGFGIHLIISR	.....
190	200
sfl:SF LTNLANPKAI YFGSVFSLFVGDNVCTTERWG FAL  VETLAWFTVVASLFA PQMRRGYQRLAKW DG	.....

>>ecc:c4745 threonine efflux protein [KO:K03329] (206 aa)  
 initn: 788 initl: 788 opt: 781 Z-score: 1097.0 bits: 198.1 E 0 : 4.3e-50  
 Smith-Waterman score: 781: 98.361% identity (98.361% ungapped) in 122 aa overlap (1-122:85-206)

10	20	30				
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL	.....	.....				
50	60	70	80	90	100	110
ecc:c4 MVWAGIALLGLHLIIEKMAWLHTI MVGGLYLCLMGYQMLRGALKKEVVSAPAPQVELAKSGRSFLKGL	.....	.....	.....	.....	.....	.....

40	50	60	70	80	90	100
eco:b3 LTNLANPKAI YFGSVFSLFVGDNVGTARWG FAL  VETLAWFTVVASLFA PQMRRGYQRLAKW DG	.....	.....	.....	.....	.....	.....
120	130	140	150	160	170	180
sfl:SF LTNLANPKAI YFGSVFSLFVGDNVCTTERWG FAL  VETLAWFTVVASLFA PQMRRGYQRLAKW DG	.....	.....	.....	.....	.....	.....

110	120
eco:b3 FAGALFAGFGIHLIISR	.....
190	200
ecc:c4 FAGALFAGFGIHLIISR	.....

>>stm:STM3959 rhtC; RhtB family, threonine efflux protein (206 aa)  
 initn: 724 initl: 724 opt: 717 Z-score: 952.6 bits: 182.5 E 0 : 2.2e-45  
 Smith-Waterman score: 717: 87.705% identity (87.705% ungapped) in 122 aa overlap (1-122:85-206)

10	20	30				
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL	.....	.....				
50	60	70	80	90	100	110
stm:ST MVWAGVALLGLHLIIEKMAWLHTI MVGGLYLCLMGYQMLRGALKKDAAASSPHIELAQSGRSFLKGL	.....	.....	.....	.....	.....	.....

40	50	60	70	80	90	100
eco:b3 LTNLANPKAI YFGSVFSLFVGDNVGTARWG FAL  VETLAWFTVVASLFA PQMRRGYQRLAKW DG	.....	.....	.....	.....	.....	.....
120	130	140	150	160	170	180
stm:ST LTNLSNPKAIIYFGSVFSLFVGDNVGAARWG FALITLETLAWFTVVASLFA PQMRRGYQRLAKW DG	.....	.....	.....	.....	.....	.....

110	120
eco:b3 FAGALFAGFGIHLIISR	.....
190	200
stm:ST FAGALFAGFGIHLIISR	.....

>>sty:STY3600 rhtC; threonine efflux protein [KO:K03329] (206 aa)  
 initn: 724 initl: 724 opt: 717 Z-score: 952.6 bits: 182.5 E 0 : 2.2e-45  
 Smith-Waterman score: 717: 87.705% identity (87.705% ungapped) in 122 aa overlap (1-122:85-206)

10	20	30				
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL	.....	.....				
50	60	70	80	90	100	110
sty:ST MVWAGVALLGLHLIIEKMAWLHTI MVGGLYLCLMGYQMLRGALKKDAAASSPHIELAQSGRSFLKGL	.....	.....	.....	.....	.....	.....

[http://www.genome.jp/tmp/get\\_linkdb\\_fasta.25159/result\\_genes.html](http://www.genome.jp/tmp/get_linkdb_fasta.25159/result_genes.html)

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R 23/ 34

Search Result: eco:b3823 -&gt; GENES

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50 60 70 80 90 100 110

40 50 60 70 80 90 100  
 eco:b3 LTNLANPKAIYFGSVFSLFVGDNVGTARWGFALIIVETLAWFTVVASLFA  
 sty:ST LTNLSNPKAIYFGSVFSLFVGDNVGAARWGFALITLETLAWFTVVASLFA  
 120 130 140 150 160 170 180

110 120  
 eco:b3 FAGALFAGFGIHLIISR  
 sty:ST FAGALFAGFGIHLIISR  
 190 200

>>st:t3338 rhtC: threonine efflux protein [KO:K03329] (206 aa)  
 initn: 724 init1: 724 opt: 717 Z-score: 852.6 bits: 182.5 E 0 : 2.2e-45  
 Smith-Waterman score: 717; 87.705% identity (87.705% ungapped) in 122 aa overlap (1-122:85-206)

10 20 30  
 eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL  
 stt:t3 VWWAGVALLGLHLIEKMAWLHTIMVGGGLYLCHMGYQMLRGALKKKDAASSPHIELAQSGRSFLKGL  
 50 60 70 80 90 100 110

40 50 60 70 80 90 100  
 eco:b3 LTNLANPKAIYFGSVFSLFVGDNVGTARWGFALIIVETLAWFTVVASLFA  
 stt:t3 LTNLSNPKAIYFGSVFSLFVGDNVGAARWGFALITLETLAWFTVVASLFA  
 120 130 140 150 160 170 180

110 120  
 eco:b3 FAGALFAGFGIHLIISR  
 stt:t3 FACALFACFGIHLIISR  
 190 200

>>eca:EC4171 rhtC: threonine efflux protein (207 aa)  
 initn: 577 init1: 533 opt: 561 Z-score: 746.8 bits: 144.4 E 0 : 6.3e-34  
 Smith-Waterman score: 561; 66.667% identity (67.213% ungapped) in 123 aa overlap (1-122:85-207)

10 20 30  
 eco:b3 MGYQMLRGALKKEAV-SAPAPQVELAKSGRSFLKG  
 eca:EC VVAAIAALLGLHLQQIAWLHTATVGGGLYLCHMGWQLRSARSQLETTQETAVVLQRGKTFMRG  
 50 60 70 80 90 100 110

40 50 60 70 80 90 100  
 eco:b3 LLTNLANPKAIYFGSVFSLFVGDNVGTARWGFALIIVETLAWFTVVASLFA  
 eca:EC LLTNLANPKAIYFGSVFSLFVGDSVGSARWGLFALISIETLLWFSLVAIVFALPTMRRGYQRLAKWVD  
 120 130 140 150 160 170 180

110 120  
 eco:b3 GFAGALFAGFGIHLIISR  
 eca:EC GVAGVLFTGFGIHLIFSR  
 190 200

>>ypm:YP3216 rhtC: threonine efflux protein (206 aa)  
 initn: 567 init1: 567 opt: 560 Z-score: 745.5 bits: 144.1 E 0 : 7.5e-34  
 Smith-Waterman score: 560; 67.213% identity (67.213% ungapped) in 122 aa overlap (1-122:85-206)

10 20 30  
 eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL  
 50 60 70 80 90 100 110

[http://www.genome.jp/tmp/get\\_linkdb\\_fasta.25159/result\\_genes.html](http://www.genome.jp/tmp/get_linkdb_fasta.25159/result_genes.html)

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SEP-07-2004 11:26 AJINOMOTO CSLLC  
2004 09/00 19:34 FAX 75-11-11-11-11-11-11

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Search Result: eco:b3823 → GENES

pmu:PM LFHALASILGLA|LFNTVPVLQQLVMTLGGGYLAYLGYLMLKS—QQNVVFEPYSEQEQNKQTSIKKEIT  
50 60 70 80 90 100 110

eco:b3 KGLLTNLANPKAI|YFGSVFSLFVGDNVGTARWGI|FAL|VETLAWFTVVASLFLAPQMRGGYQRLAKW  
40 50 60 70 80 90 100

pmu:PM KGLLVNLNAKAVIYFASVMSLVLVNLQTQWQSALLIVLETFLFYAI|SIVFCSRQQAKQFYSQYSRY  
120 130 140 150 160 170 180

eco:b3 1DGFAAGALFAGFGIHLIISR  
110 120

pmu:PM IDHLSGVIFLLFGVYLMYSGIGEMTPLISK  
190 200 210

>>pha:BH2932 unknown conserved protein (210 aa)  
initn: 221 initl: 221 opt: 229 Z-score: 308.8 bits: 63.4 E 0 : 1.6e-09  
Smith-Waterman score: 229; 32.540% identity (34.167% ungapped) in 126 aa overlap (1-120:82-207)

eco:b3 10 20  
MGYQMLRGAL-KKEAV—SAPAPQVELAKSG-R

bha:BH 1VHITYTVLGFATIETYPALFFT|QLLGAAYLIWLGPHAIRSSPPKKEEAEIEETQPIQSTKDSKSSIQ  
50 60 70 80 90 100 110

eco:b3 30 40 50 60 70 80 90  
SFLKGLLTNLANPKAI|YFGSVFSLFVGDNVGTARWGI|FAL|VETLAWFTVVASLFLAPQMRGGYQRL

bha:BH GFKEGFITNLLNPKAALFFLSIFSQFITPQTADWVRHHMYGLEVVAVGLWFSFLAFISYKHFRRFYQTH  
120 130 140 150 160 170 180

eco:b3 100 110 120  
AKWIDGFAAGALFAGFGIHLIISR

bha:BH SYWFDRFLGAALLFFAIRIIIGAF  
190 200 210

>>pst:PSPT02958 rhtC: threonine efflux protein (214 aa)  
initn: 228 initl: 229 opt: 227 Z-score: 306.1 bits: 62.9 E 0 : 2.2e-09  
Smith-Waterman score: 227; 33.628% identity (34.862% ungapped) in 113 aa overlap (12-120:93-205)

eco:b3 10 20 30 40  
MGYQMLRGALKKEAVSAPAPQ—VELAKSGRSFLKGLLTNLNP

pst:PS AATGLGLVFEQLPWLQPALQQLGGAYLTWLTQTKSLRSAGSQPKPRDVGALGIGSLSRAYRGLLTNLTP  
60 70 80 90 100 110 120

eco:b3 50 60 70 80 90 100 110  
KAIIYFGSVFSLFVGDNVGTARWGI|FAL|VETLAWFTVVASLFLAPQMRGGYQRLAKWIDGFAAGALFA

pst:PS KALAFYTSVFTTTPGMPMIVRTAGVSI|AVLAISWFVLLATLFS|PAVQARYQRMMKAIDIVTGLFWI  
130 140 150 160 170 180 190

eco:b3 120  
GFGIHLIISR

pst:PS AFGLRLLIGLLPTGVFH  
200 210

>>bms:BR1920 transporter, LysE family (212 aa)  
initn: 209 initl: 209 opt: 221 Z-score: 298.2 bits: 61.4 E 0 : 6.1e-09  
Smith-Waterman score: 221; 32.231% identity (33.621% ungapped) in 121 aa overlap (1-118:88-206)

10 20 30

Search Result: eco:b3823 -> GENES

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eco:b3

MGYQMLR-GALKKEAVSAPAPQVELAKSG--RSFL

bms:BR MMHVTYTVLGLGLIISRSIYLFIIVKWCGVAYLVYIGFKALRAGTTKIEA--GPDKEPRRKQGFKAFCG  
60 70 80 90 100 110 120

40 50 60 70 80 90 100  
eco:b3 KGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIHALIIVETLAWFTVVASLFLALPQMRRGYQLAKW  
130 140 150 160 170 180 190

110 120  
eco:b3 IDGFAGALFAGFGIHLIISR  
bms:BR IDRTSGVVFIAGLKLATEKAM  
200 210

>>bme:BME10143 threonine efflux protein (212 aa)  
initn: 209 initl: 209 opt: 221 Z-score: 298.2 bits: 61.4 E0: 6.1e-09  
Smith-Waterman score: 221: 32.231% identity (33.621% ungapped) in 121 aa overlap (1-118:88-206)

eco:b3

10 20 30  
MGYQMLR-GALKKEAVSAPAPQVELAKSG--RSFL

bme:BM MMHVTYTVLGLGLIISRSIYLFIIVKWCGVANLYVYIGFKALRAGTTKIEA--GPDKEPRRKQGFKAFCG  
60 70 80 90 100 110 120

40 50 60 70 80 90 100  
eco:b3 KGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIHALIIVETLAWFTVVASLFLALPQMRRGYQLAKW  
130 140 150 160 170 180 190

110 120  
eco:b3 IDGFAGALFAGFGIHLIISR  
bme:BM IDRTSGVVFIAGLKLATEKAM  
200 210

>>hin:HI1307 hypothetical protein HI1307 [KO:K03329] (210 aa)  
initn: 203 initl: 203 opt: 220 Z-score: 296.9 bits: 61.2 E0: 7.2e-09  
Smith-Waterman score: 220: 36.000% identity (39.474% ungapped) in 125 aa overlap (1-119:82-201)

eco:b3

10 20 30  
MGYQMLR-GALKKEAVSAPAPQVELAKSG--RSFL

hin:HI AFVGMSLGLAFLVTIPALHGVIMLLGGSYLAYLGFLMARS-KKYAKFESHSDTEFNQQTTIKKEIL  
50 60 70 80 90 100 110

40 50 60 70 80 90 100  
eco:b3 KGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIHALIIVETLAWFTVVASLFLALPQMRRGYQLAKW  
120 130 140 150 160 170 180

100 110 120  
eco:b3 AKWIDGFAGALFAGFGIHLIISR  
hin:HI SRYIDNMGAVFLFFGCVLVYNGINEIIH  
190 200 210

>>psr:PSPT01147 transporter, LysE family (210 aa)  
initn: 213 initl: 213 opt: 216 Z-score: 291.7 bits: 60.2 E0: 1.4e-08  
Smith-Waterman score: 216: 28.689% identity (28.926% ungapped) in 122 aa overlap (1-121:86-207)

## Search Result: ec9:b3823 → GENES

eco:b3 MCYQALRGALKKEAVSAPQVELAKSGR-SFLKG  
 pst:PS FVHVGYSLLGIGIIVSQSIVLFNHALKWAAYLLYIGIKALRAKPAATDDTAIKAVAGERSARGAYISG  
       60      70      80      90      100     110     120  
  
       40      50      60      70      80      90      100  
 eco:b3 LLTNLANPKAIIYFGSVFSLFVGDNVTARWGIFALIIVETLAWFTVVASLFLALPQMRRGYQRLAKWID  
 pst:PS FVTNGLNPKAATLFFLSLFTVVINPHTPLLVQGGYGVYLAVATAAWFCVLVARLFSQARVRAGFARMGHWFD  
       130     140     150     160     170     180     190  
  
       110      120  
 eco:b3 GFAGALFAGFGIHLISR  
 pst:PS RAMGGVLVALGIKLALTEVR  
       200     210

>>cdi:DIP1767 putative LysE type translocator (212 aa)  
initn: 211 initl: 211 opt: 216 Z-score: 291.6 bits: 60.2 E 0 : 1.4e-08  
Smith-Waterman score: 216; 29.839% identity (30.579% ungapped) in 124 aa overlap (1-121:85-208)

eco:b3 MGYQMLRGALKK—EAVS—APAPQVELAKSGRSFL  
 cdi:DI LVWNTLTVFGATAVLTAYPSVLSAQLVGGTLLWAGTKLVVRVARROLGEGVAVASTDALLGTPAQCYR  
 50 60 70 80 90 100 110  
 eco:b3 KGLLTNLANPKAIYFGSVFSLFVGDNVGTTRRGI|FALI|VETLAWFTVVASLFLALPCWRRGYQRLAKW  
 cdi:DI QGLATNLNSNPWKLYFAAI|APFLPTNPSLLTALSVIVVIVLSNLVMFSLLATVISTNALRRAFLKAGPW  
 120 130 140 150 160 170 180  
 eco:b3 IDGFAGALFAGFGIHLIIISR  
 cdi:DI PDLVAGCFFIAGIGLIIATRS  
 190 200 210

>>smc02484 putative amino acid efflux transmembrane protein (214 aa)  
initn: 204 initl: 204 opt: 210 Z-score: 283.7 bits: 58.7 E0: 4e-08  
Smith-Waterman score: 210; 31.967% identity (33.333% ungapped) in 122 aa overlap (1-118:88-208)

>>pr:PBPRA3511 hypothetical threonine efflux protein (218 aa)  
initn: 211 initl: 211 opt: 210 Z-score: 283.6 bits: 58.8 E(): 4e-08  
Smith-Waterman score: 210; 28.68% identity (30.172% ungapped) in 122 aa overlap (5-122:99-218)

Search Result: eco:b3823 -&gt; GENES

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eco:b3 10 20 30  
MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNL  
ppr:PB 70 80 90 100 110 120 130  
LL1HQOPTLFALLQAAGGLYLLWLGI GAVRSYLMPIFRPTAHTETVTAP—QRITANRKQALVKGFTTNI  
eco:b3 40 50 60 70 80 90 100  
ANPKAIYFGSVFSLFVGDNVGTARWG|FALIIVETLAWFTIVASLFAFPQHRRGYQRLAKWIDGFAGA  
ppr:PB 140 150 160 170 180 190 200  
LNPKALVFFISLLSTIVPVDMHSTSGKITAIAILWITSFLWFAMLAWLTTGKRLQQKIQQWTPYIDGICGV  
110 120  
eco:b3 LFAGFG—IHLIISR  
ppr:PB 210  
LFVTIGSMILLNLVAR

>>vch:VC0191 conserved hypothetical protein (222 aa)  
initn: 191 initl: 191 opt: 206 Z-score: 278.2 bits: 57.8 E 0 : 7.9e-08  
Smith-Waterman score: 206: 27.826% identity (29.091% ungapped) in 115 aa overlap (1-111:87-200)

eco:b3 10 20 30  
NGYQMLRGALKKEAVS—APAPQVELAKSGRSF  
vch:VC 60 70 80 90 100 110 120  
LVHLILSLSGISYLVKQQPHLFNLLQLAGGSYLLYLGAGALQSVMQKNASTPTHSPAPSILGNRRQAF  
eco:b3 40 50 60 70 80 90 100  
LKGLLTNLANPKAIIYFGSVFSLFVGDNVGTARWG|FALIIVETLAWFTIVASLFAFPQHRRGYQRLAK  
vch:VC 130 140 150 160 170 180 190  
TKGMNTNLLNPKALVFFVSLLSSIIPASMSVSGKVSAAAILVGLSLTWFSCLAWLTTSAMQGRMQRITR  
110 120  
eco:b3 WIDGFAGALFAGFGIHLIISR  
vch:VC 200 210 220  
SVDSICAAVFILAGGVILWQASRAIAQTFGWL

>>atu:Atu2633 rhtB; RhtB family transporter (204 aa)  
initn: 200 initl: 200 opt: 201 Z-score: 272.0 bits: 56.5 E 0 : 1.8e-07  
Smith-Waterman score: 201: 33.065% identity (35.345% ungapped) in 124 aa overlap (1-118:77-198)

eco:b3 10 20 30  
MGYQMLRGALKKEAVSAPAPQVEL-AKSGRSFLK-  
atu:At 50 60 70 80 90 100 110  
MFHVTTYTLGLGLIIQSISYLFN1VKWLGVAYLIYIGIKALR—ACKTEPLTAEGGEODGVRAKS DQTGLKA  
eco:b3 40 50 60 70 80 90  
—GLLTLANPKAIIYFGSVFSLFVGDNVGTARWG|FALIIVETLA—WFTIVASLFAFPQHRRGYQRL  
atu:At 120 130 140 150 160 170  
FTLGFAANALNPKVFFFSLFSTVVHAHPVGKFG-YGLVMASCLILWPGVGSLEMTTPRMRAAFQRA  
100 110 120  
eco:b3 AKWIDGFAGALFAGFGIHLIISR  
atu:At 180 190 200  
SQWIDRTSGVVFIALGIKLATEKAA

>>atc:AGR\_C\_4773 amino acid efflux-like protein (216 aa)  
initn: 200 initl: 200 opt: 201 Z-score: 271.8 bits: 56.6 E 0 : 1.8e-07

Smith-Waterman score: 201; 33.06% identity (35.34% ungapped) in 124 aa overlap (1-118:89-210)

eco:b3 10 20 30 MGYDMLRGALKKEAVSAPAPQVEL-AKSGRSFLK-

atc:AG NFHVTTI|LGLGLI|SQSIYLFNIVKULGVAYLIYIGIKALAR-AGKTELPTAEGGEDGVRAKSQDTGLKA  
60 70 80 90 100 110 120

40 50 60 70 80 90  
eco:b3 ---GLLTNLANPKAIYFGCSVSLFVGCDHVGTTARHGIFALIIVETLA-WFTVVASLFAFPQMRRGYQRL

atc:AG FTLGFAANALNPKPVFFFLS1FSTVWHAHTPVG1KFG-YGLVMASCL1LWFVGVSLEMTTPRNRAAFQRA  
130 140 150 160 170 180 190

100 110 120  
eca:b3 AKWIDGFAGALFAGFGIHLISR

atc:AG SQWIDRTSGVVFIALGIKLATEKAA  
200 210

>>ecc:c0448 yahN: resistance factor to homoserine/threonine, RhtB (224 aal)  
initn: 204 init1: 204 opt: 201 Z-score: 271.6 bits: 56.6 E0 : 1.9e-07  
Z-score: 271.6 bits: 56.6 E0 : 1.9e-07 ecc:c0448 is over

Smith-Waterman score: 201; 34.783% identity (37. 209% ungapped) In 92 aa overlap (31-119:129-217)

**eco:b3** MCYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNANPKAIYFGSVFSLFVGDNVGTAR

ecc:c0 GAYLLWFAWCSSMRRHSTPQMSTLQQPI SAPWVFFRRLITDLSHPQTVLFFISIFSVTLHAETPTWAR  
100 110 120 130 140 150 160

70 80 90 100 110 120  
ECO:b3 W G I F A L I I V E T L A W F T V V A S I L F A L P Q M R R G Y — Q R L A K W I D G F A G A L F A G F G I H L I I S R

ecc:00 LIAWAGIVLASIIRVFLSQAFSLPAVRRAYGRMQRVASW—(CA)IVFALRL)YEGVTQR  
170 180 190 200 210 220

>>ecj:JW0320 yahN; resistance factor to homoserine/threonine, Rht (223 aa)  
initn: 206 initl: 206 opt: 198 Z-score: 267.7 bits: 55.8 E0: 3.1e-07

Smith-Waterman score: 198; 32.584% identity (32.584% ungapped) in 89 aa overlap (31-119:128-216)

**eco:b3** MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGIIITHLANPKAIYFGSVFSLFVCDNVGTTAR

ecj : JW GGAYLLWFACSMRRQSTPQHSTLQQPISAPWYVFFRRLIITDLSNPQTVLFFISIFSVTLNAETPTWAR  
180 189 198 207 216 225 234 243 252 261 270 279 288 297 306 315 324 333 342 351 360

70 80 90 100 110 120  
85Q-b3 WGI FALI VETLAWETVYASLFA LPOMURRGYORLAKWIDFGAGALFAGFGIHLISR

ECO:DS WGPFLATTVEALWFTIVASLPLPQAKRQYQKAKNDPAPQAEPAQGPKHATTSRK  
 ecj:JW LMAGWGTVLASI||WRVFLSQAFSLPAVRAYGRMQRVASRV|GATIGVFAIRLIYEGVTQR  
 170 180 190 200 210 220

>>eco:b0328\_yahN: putative cytochrome subunit of dehydrogenase [K (223 aa)  
initn: 206 initl: 206 opt: 198 Z-score: 267.7 bits: 55.8 ED: 3.1e-07

Smith-Waterman score: 198; 32.584% identity (32.584% ungapped) in 89 aa overlap (31-119:128-216)

**eco: b3** 10 20 30 40 50 60  
MGYQWLRGALKKEAVSAPAPQVELAKSGRSFLKGULTNLANPKAIYFGSVFSLFVGDNVCTTAR

eco:b6 GGAYLLWFAWCMSMRQQSTPQMLTQQPI SAPWYVFFRQLI TDSNPQTVLFF S I FSVTLNAETPTWAR  
162 110 120 130 140 150 160

70 80 90 100 110 120  
sec:b3 WC1EAI LIVETI AWETVVASI EAI POMDRGYORLAKHNDGEAGAI FAGEGHI 11SR

SEP-07-2004 11:28 AJINOMOTO CSLLC  
ZU04 UY/UO H 19:31 PAA 万仙村可乐猪  
U4-5-201 0:44PM 2004 (EST) XUNHUA  
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eco:bo LIAWAGIVLASI IWRVFLSQAFSLPAVRRAYGRMQRVAASRIGA IGVFARLI YEGUTQR  
170 180 190 200 210 220

>>e:ZD424 yahN: putative cytochrome subunit of dehydrogenase OK (223 aa)  
initn: 206 initl: 206 opt: 198 Z-score: 267.7 bits: 55.8 E0: 3.1e-07  
Smith-Waterman score: 198: 32 58% identity (32 58% ungapped) in 89 aa overlap (31-119:128-216)

10	20	30		40	50	60
eco:b3	MGYQHLRGALKKEAVSAPAPQVELAKSGRSFLKGILTNLNPKA	IYFGSVFSLFVGDNVGTAR				
70	80	90		100	110	120
eco:Z0	GGAYLLWFAWCSNRRQSTPQHSTLQQPINA	PWYFFRRGLTDLNSNPQTVLFFSISFSVTLN	AETPTW			
130	140	150		160		

70 80 90 100 110 120  
eco:b3 WG|FAL|IVETLAWFTVVASL|FALPQMRGGYQRLAKWIDGFA|GALFGFGIHLII|SR

ece:20 LMWAGIVLASIIWAVFLSQAFSLPAVRRAYGRNQVASRVIAGAIIGVFALRLIYEGVTQR  
170 180 190 200 210 220

>>ers: ECs0382 putative cytochrome subunit of dehydrogenase [KO:K0 (223 aa)  
initn: 206 initl: 206 opt: 198 Z-score: 267.7 bits: 55.8 E0 : 3.1e-07  
Smith-Waterman score: 198; 32.584% identity (32.584% ungapped) in 89 aa overlap (31-119:128-216)

10	20	30	40	50	60
eco:b3	MGYQHILRGALIKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTAR				
100	110	120	130	140	150
ecs:EC	GGAYLLWFAWCSJRRQSTPQHNTLQQPIAPWYVFFRRGLITDLSNPQTVLFF1ISFSVTLNAEPTW				160

70 80 90 100 110 120  
eco:b3 WGIFALIVETLAWFTVVASLFLPQMRGGYQLRLAKHIDGFAGALFAGFGIHLIISR

ecs:EC LMAWAGIVLASI || WVFVLSQAFSLPAVRRAYGRMGRVASRV | GAI || GVFAFLRLI | YEGVTQR  
170 180 190 200 210 220

>>ca|NCel0143 CgID146: putative threonine efflux protein (228 aa)  
Initn: 138 initl: 138 opt: 197 Z-score: 266.3 bits: 55.6 E0: 3.7e-07  
Smith-Waterman score: 197; 35.398% identity (38.462% ungapped) in 113 aa overlap (9-119:108-213)

<b>eco:b3</b> <b>cgi:NC</b>	<b>10</b> <b>80</b>	<b>20</b> <b>90</b>	<b>30</b> <b>100</b>	<b>40</b> <b>110</b>	<b>80</b> <b>120</b>	<b>130</b>
	<b>MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGQLLTLNANPK</b> <b>... ... ... ...</b>					
	<b>LLQLVGGGYLTYMGIGAVRSWHTKRSTQQAAADSQAVENTLYTATAASGVWPAIRS—GIATNLNSPK</b>					

50	60	70	80	90	100	110
eco:b3 AI  YFGSVSLFVGDNVGTARWGI F—AI  VETLAWFTVASLFLPQURRGVQRALKWIOGFAGALF						
140	150	160	170	180	190	200
cgl:NC AVLFFGSVFAQFVRPDAGIG—WSI F GVFLTLTGLLWFVGFAVL--VRKLAAGLTRNGAI  DLLTGVIF						

120  
 eco:b3 AGFGIHLIISR  
 : : :  
 cgl:NC IGLGMFMIFEGVVGIGGRVVG  
 210 220

>>stm:STM0365\_yahn; paral putative transport protein [K0;K03329] (210 aa)  
Initn: 202 initl: 202 opt: 194 Z-score: 262.6 bits: 54.8 E(0): 5.9e-07  
Smith-Waterman score: 194; 31.461% identity (31.461% ungapped) in 89 aa overlap (31-119:115-203)

eco:b3 MGYQHLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNILANPKAIYFGSVFSLFVGDNVGTAR  
str:ST GGAYLLWFAWSNSIRHDAOTPWSTLQTPIAAPWTIFFRRGLMTDLNHPQTVLFFISFSVTLSAEPTW

Search Result: eco:b3823 → GENES

80 90 100 110 120 130 140

eco:b3 70 80 90 100 110 120  
WGIFALIIVETLAWFTVVASLFLALPQMRGGYQRLAKWIDGFAGALFAGFGIHLIISR  
stt:ST LMAHAGIVLSSVIWRIFLSQAFSLPAVRRAYGRIQR1ASRVIGAIGMFALRLLYEGMTHR  
150 160 170 180 190 200 210

>>sty:STY0397 RhtC-like transporter (210 aa)  
initn: 202 init1: 202 opt: 194 Z-score: 262.6 bits: 54.8 E0: 5.9e-07  
Smith-Waterman score: 194; 31.461% identity (31.461% ungapped) in 89 aa overlap (31-119:115-203)

eco:b3 10 20 30 40 50 60  
MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTAR  
sty:ST GGAYLLWFARNISIRHQATPQMSLQLTPIAAPVTTFFRGLMTDLSNPQTVLFFFISIFSVTSAETPTWAR  
80 90 100 110 120 130 140

eco:b3 70 80 90 100 110 120  
WGIFALIIVETLAWFTVVASLFLALPQMRGGYQRLAKWIDGFAGALFAGFGIHLIISR  
stt:ST LMAHAGIVLSSVIWRIFLSQAFSLPAVRRAYGRIQR1ASRVIGAIGMFALRLLYEGMTHR  
150 160 170 180 190 200 210

>>t2499 RhtC-like transporter (210 aa)  
initn: 202 init1: 202 opt: 194 Z-score: 262.6 bits: 54.8 E0: 5.9e-07  
Smith-Waterman score: 194; 31.461% identity (31.461% ungapped) in 89 aa overlap (31-119:115-203)

eco:b3 10 20 30 40 50 60  
MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTAR  
stt:t2 GGAYLLWFARNISIRHQATPQMSLQLTPIAAPVTTFFRGLMTDLSNPQTVLFFFISIFSVTSAETPTWAR  
80 90 100 110 120 130 140

eco:b3 70 80 90 100 110 120  
WGIFALIIVETLAWFTVVASLFLALPQMRGGYQRLAKWIDGFAGALFAGFGIHLIISR  
stt:t2 LMAHAGIVLSSVIWRIFLSQAFSLPAVRRAYGRIQR1ASRVIGAIGMFALRLLYEGMTHR  
150 160 170 180 190 200 210

>>mlo:m16377 threonine efflux protein (212 aa)  
initn: 198 init1: 172 opt: 194 Z-score: 262.6 bits: 54.8 E0: 5.9e-07  
Smith-Waterman score: 194; 30.400% identity (31.405% ungapped) in 125 aa overlap (1-122:88-211)

eco:b3 10 20 30  
MGYQMLRGAL—KKEAVSAPAPQVELAKSGRSFL  
mlo:m1 IFWGFMASTG1SALLARYAQALLVLQVFGGLYLLFLAFRAGRSALTSNEKLAVRASTDQVALSR-GELYR  
60 70 80 90 100 110 120  
40 50 60 70 80 90 100  
eco:b3 KGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIFALIVETLAWFTVVASLFLALPQMRGGYQRLAKW  
mlo:m1 KGLLMHLANPKSVLAHIALVTLG1GPNSWQSIAILGGCAILSVTIFCGYA1VFSTPPMVALYRRCRRW  
130 140 150 160 170 180 190  
110 120  
eco:b3 IDGFAGALFAGFGIHLIISR  
mlo:m1 IESLLAMFFAFAGLRMILLSRW  
200 210

>>pae:PA4757 conserved hypothetical protein [KO:K03329] (216 aa)  
initn: 152 init1: 112 opt: 192 Z-score: 259.9 bits: 54.4 E0: 8.4e-07  
Smith-Waterman score: 192; 36.000% identity (39.130% ungapped) in 125 aa overlap (1-118:89-210)

>>ae:PA2929 hypothetical protein (204 aa)  
initn: 190 initl: 190 opt: 191 Z-score: 258.8 bits: 54.1 E0: 9.6e-07  
Smith-Waterman score: 191; 31.356% identity (31.897% ungapped) in 118 aa overlap (1-118:84-199)

eco:b3 MGYQMLRGALIKKEAVSAPAQVELAKSGRSFLKGL  
 pae:PA TVHVGYSILGVGVLVRESLALFTALKLAGAAYLVFLGLPULLA—REDSVAAEAAAGGAGVSSWAMLRSGF  
 50 60 70 80 90 100 110  
 eco:b3 LTNALANPKAIYFGSVFSLFVGDNVGTARHGIFALIIVETLAWFTVVASLFAFPQURRGYQLAKWIDG  
 pae:PA LTNALNPKTCLFVVSLFMQVIDPHTALPAQLGYGAFIALAHVAWFLVACFLSSPAVRGRLLRFRRRIDQ  
 120 130 140 150 160 170 180  
 eco:b3 FAGALFAGFGIHLLISR  
 pae:PA FFGALLVGFGVLLGAKSP  
 190 200

>>>PBPRA1361 hypothetical homoserine/homoserine lactone efflux (209 aa)  
initn: 178 initl: 178 opt: 191 Z-score: 268.7 bits: 54.1 E(0): 9.7e-07  
Smith-Waterman score: 191; 37.113% identity (40, 449% ungapped) in 97 aa overlap (30-122;116-208)

	10	20	30	40	50	60	
eco:b3	MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGTLTNLANPKAI	YFGSVFSLFVGDN	~VGT				
ppr:PB	VYLFWLGVSNIKNGLNISLLKFDSSQNTKKTSI	NSFFKGLLTNLNPKIVLFYLSIFPQFISPQHILAQ					
	90	100	110	120	130	140	150
	70	80	90	100	110	120	
eco:b3	TARWGIHALIIIVETLAWFTVVASLFA—LPQMRRGYQRLAKWIDGFAGALFAGFGIHLISR						
ppr:PB	SMALGITHALVVAS—WFLWVI-LFSVRLKSMLTS-SKVAKWLNVSGGLFISFGVTLASTRL						
	160	170	180	190	200		

>>cef:CE0145 conserved hypothetical protein (234 aa)  
initn: 149 initl: 149 opt: 191 Z-score: 258.2 bits: 54.2 E 0 : 1e-06  
Smith-Waterman score: 191: 35.922% identity (38.947% ungapped) in 103 aa overlap (19-179:125-221)

eco:b3 10 MGYQMLRGALI**K**EAVSAPAPQVELAKSGRSFLKGLLTNLANPKA**I**YFGSVFS.  
 cef:CE VRSWWGQR**I**TAROAGDAVERVLEGDGSDGVPGFFGSPGV**L**GAR—RALRTG**I**ATNLNSNPKAVLFFGSVFA

	90	100	110	120	130	140	150
eco: <b>b3</b>	60	70	80	90	100	110	120
	LFVGDNVGTTARWCIF--ALIIVETLAWFTTVVASLFA	PQMRRGYQRLAKWIDGFAGALFAGFGIHLIIS					
cef:CE	160	170	180	190	200	210	220
	QF1TPDHCVG-W51FLAVFLILYGLVWFLGFAVLVRSFAAR—ITRNAAVIDLFTGVIFIALGFMVWQ						

eco:**b3** R

cef:CE GVVGIGSWILG  
 230

>>eca:ECA3867 putative LysE-type translocator (204 aa)  
 initn: 180 init1: 180 opt: 190 Z-score: 257.5 bits: 53.8 E 0 : 1.1e-06  
 Smith-Waterman score: 190; 30.545% identity (33.043% ungapped) In 124 aa overlap (1-120:85-203)

	10	20	30
eco: <b>b3</b>	MGYQML—RGALKKEAVSAPAPQVELAKSGRSFLK		
eca:EC	ATHMAYCVAGLAVVITTPWLFNVLKYAGAAYLIWIGIQLALFTRGGSIQDVSNLTQQSVSLKKA—FLQ		
	50 60 70 80 90 100 110		
eco: <b>b3</b>	GLLTNLNLPKAIYFGSVFSLFVGDNVGTAR-WG1FALII-VETLAWFTTVVASLFA	PQMRRGYQRLAK	
eca:EC	120 130 140 150 160 170 180	QALFTRGGSIQDVSNLTQQSVSLKKA—FLQ	

	110	120
eco: <b>b3</b>	WIDGFAGALFAGFGIHLIISR	
eca:EC	190 200	LVDKLLGTVLIALGIKVALG

>>pae:PA4507 hypothetical protein (210 aa)  
 initn: 197 init1: 116 opt: 182 Z-score: 246.8 bits: 51.9 E 0 : 4.5e-06  
 Smith-Waterman score: 182; 35.294% identity (42.857% ungapped) In 136 aa overlap (1-122:83-208)

	10	20	30
eco: <b>b3</b>	MGYQMLRG—ALK-KEAVSAPA-PQVELAKSGRS		
pae:PA	ACHVLMATGLALLFRTAPWTFDLVRLLGAYVLAWLGLQMLRGGLALPTSDAGSAPVPHADR—RA		
	50 60 70 80 90 100 110		
eco: <b>b3</b>	FLKGLLTNLNPKAIIYFGSVFSLFVGDNVGTAA-RWG1FALII-VETLAWFTTVVASLFA	PQMRRGY—	
pae:PA	120 130 140 150 160 170 180	QALFTRGGSIQDVSNLTQQSVSLKKA—YALAGGRILGRWLA	

	100	110	120
eco: <b>b3</b>	—QRLAKWIDGFAGALFAGFGIHLIISR		
pae:PA	190 200 210	SRPRAQRLLQQW—GFGG-LIIGFGVRLLRQL	

>>cvi:CV3240 rhtC; Threonine efflux protein (207 aa)  
 initn: 171 init1: 171 opt: 181 Z-score: 245.6 bits: 51.6 E 0 : 5.2e-06  
 Smith-Waterman score: 181; 25.620% identity (25.833% ungapped) In 121 aa overlap (1-120:86-206)

	10	20	30
eco: <b>b3</b>	MGYQMLRGALKK-EAVSAPAPQVELAKSGRSFLKG		
	110 120		

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6004 03/00 13:00 RNA 7/14/2004 11:29

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cvl:CV GLYALAAAQGLAMVMAHPLLKIISSLGAAYLVWLGVQQLRAASRPARAASGETAAAPTSWRAARTG  
60 70 80 90 100 110 120

eco:b3 40 50 60 70 80 90 100  
LLTNLANPKAIYFGSVFSLFVGDNVGTARWGIHALIIVETLAWFTVVASLFLALPQMRGGYQRLAKWID  
130 140 150 160 170 180 190

110 120  
eco:b3 GFAGALFAGFGIHLIISR  
200  
cvl:CV GCGGALMLLGLRLILVV

>>son:S00765 threonine efflux protein, putative (234 aa)  
initn: 184 initl: 184 opt: 180 Z-score: 243.7 bits: 51.5 E 0 : 6.7e-05  
Smith-Waterman score: 180; 26.316% identity (27.027% ungapped) in 114 aa overlap (9-119:115-228)

eco:b3 10 20 30 40  
MGYQMLRGALKKEAVSAPAPQVELAKS—GRSFLKGLLTNLA

son:S0 ASYLAVMGMFGALKATIAFFRKPKRLLKGEEAESSVATEAQANTGDNSQTKAEKSLSPRGFMGLYTNL  
80 90 100 110 120 130 140

eco:b3 50 60 70 80 90 100 110  
NPKAIIYFGSVFSLFVGDNVGTARWGIHALIIVETLAWFTVVASLFLALPQMRGGYQRLAKWIDGFAGAL

son:S0 NPKAIVFFTLFSALITPSVTPATKVAAALVLVLSLWFGFLALMUSKAKVQQKMKQRITPIIDAVIGVI  
150 160 170 180 190 200 210

120  
eco:b3 FAGFGIHLIISR  
220 230  
son:S0 FMSVALAVSNLLV

>>cef:CE2245 putative threonine efflux protein (224 aa)  
initn: 222 initl: 177 opt: 179 Z-score: 242.8 bits: 51.2 E 0 : 7.7e-06  
Smith-Waterman score: 198; 28.462% identity (31.092% ungapped) in 130 aa overlap (1-119:85-214)

eco:b3 10 20  
MGYQMLRGALKK—EAVSAPAPQ—VEL

cef:CE TVWVTLTVVGAATLLTTYPDILGVIQLVGGGYLTWGYRMGRGAVRELLDARAFRFNSATRPIPDAVAAL  
50 60 70 80 90 100 110

eco:b3 30 40 50 60 70 80 90  
AKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIHALIIVETLAWFTVVASLFLALPQMR

cef:CE GTPGQAYRQQMATNLSNPKVINYFAALAPLMPANPSLAVALTIIAIIVQTNVVFTFCIVSTERIRK  
120 130 140 150 160 170 180

100 110 120  
eco:b3 GYRLAKWIDGFAGALFAGFGIHLIISR

cef:CE AVLRAFPVFDGVAAVFIAVGLTLIYEGASQLLG  
190 200 210 220

>>plu:plu1236 unnamed protein product; similar to amino acid effl (211 aa)  
initn: 177 initl: 177 opt: 178 Z-score: 241.5 bits: 50.9 E 0 : 8e-06  
Smith-Waterman score: 178; 26.230% identity (27.350% ungapped) in 122 aa overlap (1-119:88-207)

eco:b3 10 20 30  
MGYQMLRGALKKEAVSAPAPQVELAKSG-RSFLKG

[http://www.genome.jp/tmp/get\\_linkdb\\_fasta.25159/result\\_genes.html](http://www.genome.jp/tmp/get_linkdb_fasta.25159/result_genes.html)

2004/08/25

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